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PATENT APPLICATION: US/09/931,186

DATE: 08/23/2001

TIME: 17:09:29

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3 <110> APPLICANT: ABREO, MELWYN A.
 4 AGREE, CHARLES S.
 5 AUST, ROBERT
 6 KISSINGER, CHARLES R.
 7 MARGOSIAK, STEVE
 8 MENG, JERRY J.
 9 PELLETIER, LAURA A.
 10 REJTO, PAUL A.
 11 SHOWALTER, RICHARD E.
 12 TEMPICZYK-RUSSELL, ANNA
 13 THOMSON, JIM
 14 VANDERPOOL, DARIN
 15 VILLAFRANCA, J. ERNEST
 17 <120> TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
 18 STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
 19 OF INHIBITORS THEREOF
 21 <130> FILE REFERENCE: 0125-0049
 23 <140> CURRENT APPLICATION NUMBER: US/09/931,186
 24 <141> CURRENT FILING DATE: 2001-08-17
 26 <160> NUMBER OF SEQ ID NOS: 24
 28 <170> SOFTWARE: PatentIn Ver. 2.1
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 786
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
 35 <220> FEATURE:
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61 <223> OTHER INFORMATION: full length mutant ERAB C214R

63 <400> SEQUENCE: 2

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67 Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala Glu Arg Leu Val Gly
68           20           25           30
70 Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu
71           35           40           45
73 Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp
74           50           55           60
76 Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly
77   65           70           75           80
79 Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val
80           85           90           95
82 Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu
83           100          105          110
85 Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val
86           115          120          125
88 Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly
89           130          135          140
91 Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu
92 145           150           155           160
94 Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val
95           165           170           175
97 Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg
98           180          185          190
100 Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser
101           195          200          205
103 Leu Pro Glu Lys Val Arg Asn Phe Leu Ala Ser Gln Val Pro Phe Pro
104           210          215          220
106 Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile
107 225           230           235           240
109 Ile Glu Asn Pro Phe Leu Asn Gly Glu Val Ile Arg Leu Asp Gly Ala
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112 Ile Arg Met Gln Pro
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127 gacctgcccc actcgggtgg ggaggcccaa gccagaagt taggaaacaa ctgcgttttc 180
128 gccccagccg acgtgacctc tgagaaggat gtgcaaacag ctctggctct agcaaaagga 240
129 aagtttgccc gtgtggatgt agctgtcaac tgtgcaggca tcgcgtggc tagcaagacg 300
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133 ggtcagggtt gacaagctgc atactctgct tccaaggggg gaatagtggg catgacactg 540
134 cccattgctc gggatctggc tcccataggt atccgggtga tgaccattgc cccagggtctg 600
135 tttggcaccc cactgctgac cagcctccca gagaaagtgt gcaacttctt ggccagccaa 660
136 gtgcccttcc ctageccgact gggtgaccct gctgagtatg ctcacctcgt acaggccatc 720
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141 <210> SEQ ID NO: 4

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146 <220> FEATURE:

147 <223> OTHER INFORMATION: full length mutant ERAB C5V

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154           20           25           30
156 Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu
157           35           40           45
159 Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp
160           50           55           60
162 Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly
163   65           70           75           80
165 Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val
166           85           90           95
168 Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu
169           100          105          110
171 Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val
172           115          120          125
174 Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly
175           130          135          140
177 Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu
178   145          150          155          160
180 Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val
181           165          170          175
183 Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg
184           180          185          190
186 Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser
187           195          200          205
189 Leu Pro Glu Lys Val Cys Asn Phe Leu Ala Ser Gln Val Pro Phe Pro
190           210          215          220
192 Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile
193   225          230          235          240
195 Ile Glu Asn Pro Phe Leu Asn Gly Glu Val Ile Arg Leu Asp Gly Ala
196           245          250          255
198 Ile Arg Met Gln Pro
199           260

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215 aagtttggcc gtgtggatgt agctgtcaac tgtgcaggca tcgcggtggc tagcaagacg 300
216 tacaacttaa agaaggcca gaccataacc ttggaagact tccagcgagt tcttgatgtg 360
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220 cccattgctc gggatctggc tcccataggt atccgggtga tgaccattgc cccaggctcg 600
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222 gtgcccttcc ctagccgact gggtgaccct gctgagtatg ctcacctcgt acaggccatc 720
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228 <211> LENGTH: 261
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232 <220> FEATURE:
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239 Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala Glu Arg Leu Val Gly
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243 35 40 45
245 Ala Gln Ala Lys Lys Leu Gly Asn Asn Val Val Phe Ala Pro Ala Asp
246 50 55 60
248 Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly
249 65 70 75 80
251 Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val
252 85 90 95
254 Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu
255 100 105 110
257 Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val
258 115 120 125
260 Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly
261 130 135 140
263 Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu
264 145 150 155 160
266 Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val

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267          165          170          175
269 Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg
270          180          185          190
272 Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser
273          195          200          205
275 Leu Pro Glu Lys Val Cys Asn Phe Leu Ala Ser Gln Val Pro Phe Pro
276          210          215          220
278 Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile
279 225          230          235          240
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284 Ile Arg Met Gln Pro
285          260
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314 <211> LENGTH: 261
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316 <213> ORGANISM: Homo sapiens
318 <220> FEATURE:
319 <223> OTHER INFORMATION: wild type ERAB
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329 35 40 45
331 Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp
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VERIFICATION SUMMARY

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